

**A.**

EAEC 55989



GOS1

**B.**

EAEC 55989



GOS2

**Fig. S2** Contig order of the genomes of *E. coli* GOS1 (A) and GOS2 (B). Contig order was predicted by employing the Mauve Multiple Genome Alignment tool (<http://asap.ahabs.wisc.edu/mauve/>). Each genome is laid out horizontally and homologous segments are shown as colored blocks that are connected across genomes. Blocks that are shifted downward in any genome represent segments that are inverted relative to the reference genome *E. coli* strain 55989 (top panel).